Online-Only Abstract

Analysis of differentially expressed proteins involved in hand, foot and mouth disease and normal sera

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Abstract

We implemented 2-D DIGE technology on proteins prepared from serum obtained from children with hand, foot and mouth disease (HFMD) and controls, to study the differentially expressed proteins in control and HFMD serum samples. Proteins found to be differentially expressed were identified with matrix-assisted laser desorption/ionization time-of-flight/ time-of-flight mass spectrometry (MALDI-TOF/TOF MS) analysis. We identified 30 proteins from mild HFMD samples and 39 proteins from severe HFMD samples, compared with the normal controls. 25 proteins among them (14 up-regulated and 11 down-regulated proteins) are found in both HFMD groups. Classification analysis and protein–protein interaction map showed that they associate with multiple functional groups, including transporter activity and atalytic activity. These findings build up a comprehensive profile of the HFMD proteome and provide a useful basis for further analysis of the pathogenic mechanism and the regulatory network of HFMD.